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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/087,667

DATE: 03/14/2002

TIME: 14:06:12

Input Set : A:\Uvm-0001.app

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3 <110> APPLICANT: Bramley, John A.
 4 Plaut, Karen I.
 5 Kerr, David
 7 <120> TITLE OF INVENTION: TREATMENT OF STAPHYLOCOCCUS INFECTIONS
 9 <130> FILE REFERENCE: Mastitis
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/087,667
 12 <141> CURRENT FILING DATE: 2002-02-28
 14 <160> NUMBER OF SEQ ID NOS: 10
 16 <170> SOFTWARE: PatentIn Ver. 2.1
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 19 <211> LENGTH: 1486
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Staphylococcus simulans
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 26 gtgtgttgtt atatttcatac aaaatcaatc aatattattt tactttcttc atcgaaaaaa 180
 27 aatgtatat ttataaaaaat atgctattct cataaatgtt ataataaaattt aggaggtatt 240
 28 aagggtgaag aaaacaaaaaa acaattatta tacgagacct ttagctattt gactgagttac 300
 29 atttgcctta gcatctattt tttatggagg gattcaaaat gaaacacatg cttctgaaaa 360
 30 aagtaatatg gatgttcaa aaaaagtagc tgaagtagag acttccaaag ccccagttaga 420
 31 aaatacagct gaagttagaga ctccaaaagc tccagtagaa aatacagctg aagtagagac 480
 32 ttccaaaagct ccagtagaaaa atacagctga agtagagact tccaaaagctc cagtagaaaa 540
 33 tacagctgaa gtagagactt caaaagctcc ggtagaaaaat acagctgaag tagagacttc 600
 34 aaaagccccca gtagaaaaata cagctgaagt agagacttca aaagccccgg ttccaaaatag 660
 35 aacagcttta agagctgca cacatgaaca ttccagcacaa tgggttgaata attacaaaaaa 720
 36 aggatatggt tacggccctt atccatttagg tataaatggc ggtatgcact acggagttga 780
 37 ttttttatg aatattggaa caccagtaaa agctatttca agcggaaaaaa tagtgaagc 840
 38 tgggtggagt aattacggag gaggtaatca aataggtctt attgaaaaatg atggagtgca 900
 39 tagacaatgg tatatgcata taagtaaata gtaggagatt gtaggagatt atgtccaaagc 960
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 41 ccaaagaatg gttaaatccat ttccaaattt aactgccccaa gatccaatgc ctttctttaaa 1080
 42 gagcgcagga tatggaaaaag caggtggtagt agtaactcca acgcccgaata caggtggaa 1140
 43 aacaaacaaa tatggcacac tatataaaatc agagttagt agcttcacac ctaatacaga 1200
 44 tataataaca agaacgactg gtccatttag aagcatgccg cagtcaggag ttctaaaaagc 1260
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 46 tacaggtaac agtggccaaac gtatcttgcctgtt gatggaaata acatggaaata aatctactaa 1380
 47 tacttttaggt gttcttggg gaactataaa gtgagcgcgc ttttataaa ctttatatgtt 1440
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 53 <212> TYPE: PRT
 54 <213> ORGANISM: Staphylococcus simulans

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 63 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
 64 35 40 45
 66 Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val
 67 50 55 60
 69 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
 70 65 70 75 80
 72 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
 73 85 90 95
 75 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
 76 100 105 110
 78 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
 79 115 120 125
 81 Val Glu Thr Ser Lys Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala
 82 130 135 140
 84 Ala Thr His Glu His Ser Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr
 85 145 150 155 160
 87 Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly
 88 165 170 175
 90 Val Asp Glu Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser
 91 180 185 190
 93 Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Asn Gln
 94 195 200 205
 96 Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Glu Tyr Met His
 97 210 215 220
 99 Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln
 100 225 230 235 240
 102 Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu
 103 245 250 255
 105 His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp
 106 260 265 270
 108 Pro Met Pro Phe Leu Lys Ala Ser Gly Tyr Gly Lys Ala Gly Gly Thr
 109 275 280 285
 111 Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
 112 290 295 300
 114 Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
 115 305 310 315 320
 117 Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
 118 325 330 335
 120 Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
 121 340 345 350
 123 His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
 124 355 360 365
 126 Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp
 127 370 375 380

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 130 385
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 135 <212> TYPE: DNA
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 138 <400> SEQUENCE: 3
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 141 attggAACACAG cagtaaaAGC tatttcaAGC ggaaaaATAG ttgaagCTGG ttggagtaat 180
 142 tacggaggAG gtaatcaaAT aggtcttatt gaaaATGAT gagtgcataG acaatggta 240
 143 atgcataCTAA gtaaatataA tgtaaAGTA ggagattAT tcaaagCTGG tcaaataATC 300
 144 ggTTGGTCTG gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360
 145 aactcatTTT cacagtcaac tgcccaagat ccaatgcctt tcttaaAGAG cgccaggat 420
 146 ggaaaAGCAG gtggTACAGT aactccaaACG ccgaatacAG gttggAAAAC aaacaAAAT 480
 147 ggcacactat ataaatcaga gtcagctaG ttcacaccta atacagatAT aataacaAGA 540
 148 acgactggTC catttagaAG catGCCGCAg tcaggAGtCT taaaAGCAGG tcaaacaATT 600
 149 cattatgatG aagtGatGAA acaagacGGT catGTTGGG tagGttatac aggtAACAGT 660
 150 ggccaacGTA ttacttgcc tgtgagaaca tggcagaAGT ctactaatac tctgggtgtt 720
 151 ctgtggggAA ctataaAGTG a 741
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 155 <211> LENGTH: 1520
 156 <212> TYPE: DNA
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 162 atttgaacgt gcgtcgacg acagcgctgc gcccgcggc agagtccggc gcccgcggta 180
 163 tacggacagc gatcgccgcg tccgcgcatt acgaacggc gtgcgcgtca gtgcgcattgc 240
 164 ccgcgcgcg ctggcggtcc ggcttcgcgg ggcgcagcgcg gtccaccact ctccaaacgt 300
 165 ctttctcggg agcagcatat gaagaagatt tccaaggcgg gactgggct ggcgtcggt 360
 166 tgccgcgtgg cgacgatcgg cggcaacgcg cgcgcgcagg ccacggctca gcgccgagga 420
 167 tctggtgtat tctacgacg aatgttcgcac ttgcacatcg atgcgcatttgc ggcacgcatt 480
 168 gccgcgcatt tcgcacaagca ctccggaaAGAG atctcgcaCT gggccggcta cagcgggatc 540
 169 agccgaagtG ttgatcgcc tgatggagca gcagagcgcg cggtcacgc aagcgcgcga 600
 170 cgaatcgtcc gttcggcaag ctggcgccgc ccgcgcgtt cggcgcgcag acccgcgagg 660
 171 tcgcgcgtgg gctgcgcgag tcgcgttacg agcgcgcatttgc cgcacgcgcac agggccgg 720
 172 gacgcgtggcc cgcgcatttgc cgcgcgcgc gctttcgag cgttccgcgc acaacgagcc 780
 173 ggccgcgcgc ctgcgcgcgc acggcgagg ccagctggc tacggccgc tggtaacgc 840
 174 accgcgcgcag gccaaggcgg ctgcgcgcgc cttcgccaa gccggccgg acgtgcgc 900
 175 gtgtcgccca acggcgtgtc gcaGTTCCCC ttccgcgcg ggcgcagctg gcatgtcg 960
 176 ggcgcgcaca ccaacaccgg ctccggcaat taccgcgtt cgtcgcttgg catgtcgcc 1020
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198 20 25 30
200 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
201 35 40 45
203 Ala Glu Val Glu Thr Ser Lys Pro Pro Val Glu Asn Thr Ala Glu Val
204 50 55 60
206 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
207 65 70 75 80
209 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
210 85 90 95
212 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
213 100 105 110
215 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
216 115 120 125
218 Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr
219 130 135 140
221 Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala
222 145 150 155 160
224 Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu
225 165 170 175
227 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
228 180 185 190
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231 195 200 205
233 Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys
234 210 215 220
236 Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala Ala Thr His Glu His
237 225 230 235 240
239 Ser Ala Gln Trp Leu Asn Asn Tyr Lys Tyr Gly Tyr Gly Tyr Gly Pro
240 245 250 255
242 Tyr Pro Leu Gly Ile Asn Gly Gly Ile His Tyr Gly Val Asp Phe Phe
243 260 265 270
245 Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val
246 275 280 285
248 Glu Ala Gly Trp Ser Asn Tyr Gly Gly Asn Gln Ile Gly Leu Ile
249 290 295 300
251 Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr
252 305 310 315 320
254 Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp
255 325 330 335

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257 Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg
258 340 345 350
260 Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe
261 355 360 365
263 Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr
264 370 375 380
266 Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser
267 385 390 395 400
269 Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr
270 405 410 415
272 Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln
273 420 425 430
275 Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val
276 435 440 445
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301 35 40 45
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327 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
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VERIFICATION SUMMARY
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